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Research Article

On the occurrence of *Mulloidichthys ayliffe* Uiblein, 2011 (Indian mimic goatfish) (Teleostei: Mullidae) in the Lakshadweep Archipelago, Eastern Arabian Sea (Western Indian Ocean)

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The goatfish species *Mulloidichthys ayliffe* Uiblein, 2011 (Mullidae) is reported for the first time from the Lakshadweep Archipelago, Eastern Arabian Sea, based on morphological and genetic studies of four specimens collected off Agatti Island. The fish is characterised by a distinct pattern of 4-5 blue stripes alternating with yellow, with the dorsal-most blue stripe crossing the lateral line beyond the base of the first dorsal fin, and the presence of 37 lateral line scales. The mitochondrial *COI* gene sequence of one *M. ayliffe* specimen was compared with two other sequences of *M. ayliffe* from South African waters, and found to be matching.

[**Keywords**: Arabian Sea, Goatfish, Lakshadweep, *Mulloidichthys ayliffe*]

Introduction

The ocean depths and coral ecosystems deserve enhanced attention from taxonomists. There have been numerous accounts of fishes from Lakshadweep, but there aren't many about goatfishes (Mullidae). Currently, 103 goatfish species belonging to six genera, namely *Mulloidichthys* Whitley, 1929, *Mullus* Linnaeus, 1758, *Parupeneus* Bleeker, 1863, *Pseudupeneus* Bleeker, 1862, *Upeneichthys* Bleeker, 1853 and *Upeneus* Cuvier, 1829, are known[1]. Members of the family Mullidae occur mostly in subtropical and tropical waters and are ecologically and commercially important, frequently inhabiting shallow locations associated with coral reefs[2]. Many goatfish species can be easily identified by their bright colours when fresh and by the presence of two long, unbranched barbels on the chin. High morphological variability[3] and diverse colour patterns, including body stripes, are typical characteristics of the Mullidae family. Morphological characters such as tooth pattern, presence or absence of vomer and palatine teeth, and the arrangement of teeth on jaws can be used for identification at the genus level[4,5].

The genera within the family Mullidae are primarily distinguished by their dentition. In the genus *Mulloidichthys*, the vomer and palatine bones are toothless, while villiform teeth are arranged in multiple rows on both jaws[5]. The genus *Mulloidichthys* is represented worldwide by seven valid species, with four species from India[4-8]. Species within this genus differ significantly in terms of morphometric, meristic, and colour patterns.

Mulloidichthys ayliffe Uiblein, 2011 was previously known from Natal, South Africa, Tanzania, Kenya, Oman, Seychelles, Sri Lanka and Andaman Islands of the Western and Northeastern Indian Ocean[4]; *M. dentatus* Gill, 1862 from the eastern Pacific[9-11]; *M. flavolineatus* (Lacepède, 1801), *M. pfluegeri* (Steindachner, 1900) and *M. vanicolensis* (Valenciennes, 1831) from the Indo Pacific region[4,9,10,12]; *M. mimicus* Randall & Guézé, 1980 from the Southern Pacific; and *M. martinicus* (Cuvier, 1829) from the Atlantic Ocean[4,9,10,13].

Mulloidichthys ayliffe was first described by Uiblein[4] based on collections from the Western Indian Ocean (type locality off KwaZulu-Natal, South Africa). This present study reports an extended distribution of *M. ayliffe* from the Lakshadweep Archipelago (in the following named Lakshadweep or Laccadives), located at a distance of approximately 220 – 400 km westwards of the southwestern coast of India (8° and 12°30′ N latitude and 71° and 74° E longitude), a biodiverse rich area of 36 small islands scattered over a land area of 32 km[2](ref. 14) (Fig. 1).

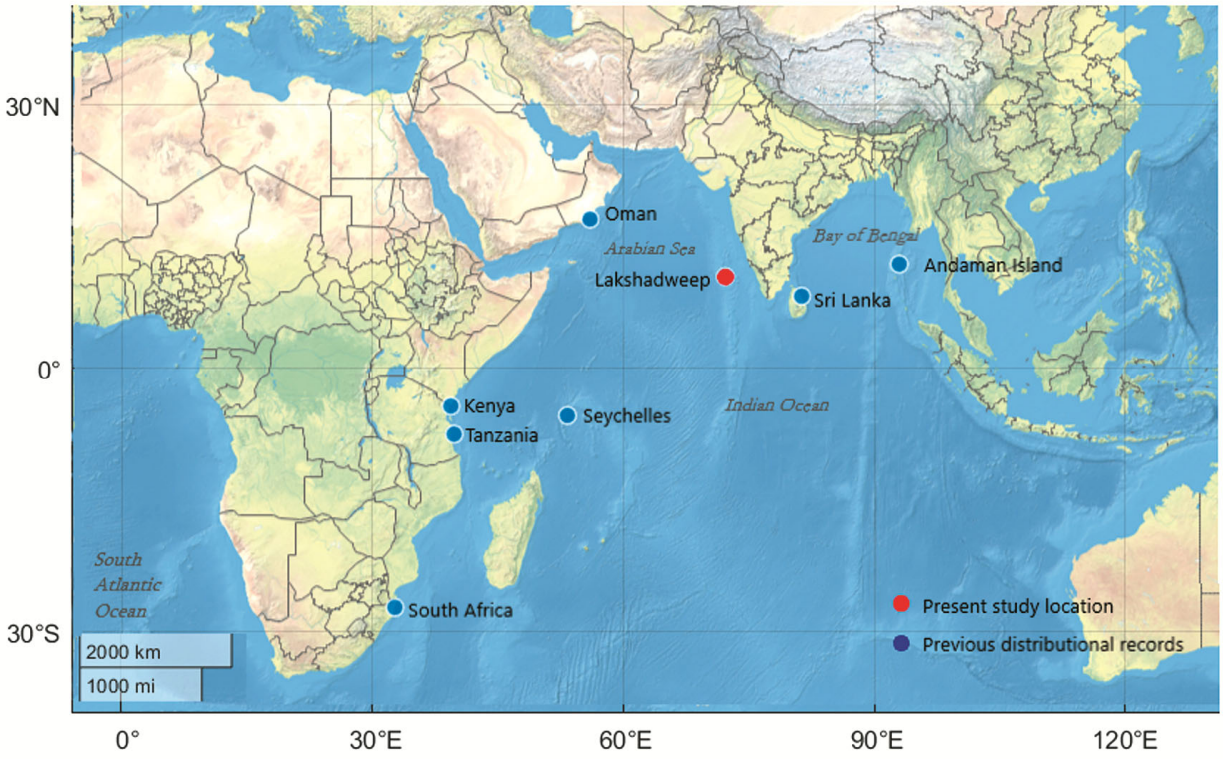

Fig. 1 — Map showing distributional record of *Mulloidichthys ayliffe*

This island group has 20,000 km² of lagoons and 4000 km² oceanic zones[14]. Documentations of the fishes of the Laccadives started with Alcock[15], Jones & Kumaran[16] and continued with Murty[17–19], Koya *et al.*[20], Nair & Kuriakose[21], Rajan *et al.*[22], and was continued recently by Sandra *et al.*[23]. These studies indicate that approximately fourteen species of goatfishes have been reported from the Lakshadweep archipelago. These studies are significant due to having added previously unreported species to the known biodiversity of the Indian seas. The occurrence of *M. ayliffe* from Agatti Island, Lakshadweep is confirmed here based on morphometric and meristic analysis and accompanying genetic studies.

Materials and Methods

Sampling locality

On December 12, 2020, four goatfish specimens measuring 123, 143, 153 and 155 mm Standard Length (SL) were collected using shore seines off the Lakshadweep (10°48′40.9″ N, 72°9′56.6″ E), at depths from 5 – 10 m. One fish specimen was photographed in fresh condition. The specimens were thereafter taken to the biology lab of the Central Marine Fisheries Research Institute (CMFRI), Kochi (Western Indian coast) for morphometric and meristic analyses. The muscle tissue was taken from a specimen of SL143 mm for molecular analysis, and then kept in a freezer at -18 °C. The fish were tentatively identified as *Mulloidichthys ayliffe* based on Uiblein[4]. A voucher specimen (SL of 143 mm) has been deposited at the Designated National Repository (DNR) Museum of Central Marine Fisheries Research Institute (CMFRI) (Accession No. GB.31.95.1.3).

Measurements and counts

Fish length was determined by Standard Length (SL) following Uiblein[4]. The fishes were studied and finally identified by consulting the original description by Uiblein[4]. Measurements were made using a digital caliper (make Mitutoyo CD-6”ASX) and recorded to the nearest 0.01 mm. Body weight was measured in grams with the help of an electronic balance (Saffron Electronic Scale SES3T). The following characters were examined: morphometric measurements: SL, body depth at first dorsal-fin origin, body depth at anal-fin origin, half body depth, half body depth at anal fin origin, Caudal-Peduncle Depth (CPD), caudal-peduncle width at position of CPD measurement, maximum head depth, head depth across a vertical midline through eye, suborbital

depth, interorbital length, head length, snout length, postorbital length, orbit length, horizontal fleshy orbit diameter, orbit depth, upper-jaw length, lower-jaw length, snout width, barbel length, maximum barbel width, first pre-dorsal length, second pre-dorsal length, interdorsal distance, caudal-peduncle length, pre-anal length, pre-pelvic length, pre-pectoral length, second dorsal-fin depth, pelvic-fin depth, pectoral-fin depth, length of first dorsal-fin base, length of second dorsal-fin base, caudal fin length, length of anal-fin base, anal fin height, pelvic-fin length, pectoral-fin length, width of pectoral-fin base, first dorsal-fin height, second dorsal-fin height; meristic counts: number of pectoral-fin rays, gill rakers, and lateral line scales; in addition, the position of the crossing point of the blue dorso-mid-lateral body stripe and lateral line, and wet weight (g) were recorded. For comparative studies, morphometric dimensions were converted into percentages of standard length, head length and the ratio of standard length.

Molecular analysis

DNA sequencing was done to confirm the species identification. Genomic DNA was extracted from the tissue using the Phenol-Chloroform method[24]. PCR amplification of the mitochondrial gene (*COI*) was carried out with primers Fish F1 and Fish R1 using standard protocols[25]. All the PCR reactions were performed in 25 µl, containing 12.5 µl of EmeraldAmp GT PCR Master Mix, 0.5 µl of each primer and 2 µl of 50 ng/µl DNA template. The PCR amplifications were carried out in BIORAD T100 thermal cycler (Biorad, USA) under the PCR conditions of Initial denaturation at 94 °C for 4 min, 30 cycles of denaturation for 30 s at 94 °C, 40 s of annealing at 42 °C, 45 s of extension at 72 °C, and a final extension of 7 min at 72 °C. Purified samples were visualised on agarose gel electrophoresis (2 %) containing ethidium bromide. Sequencing was done by the Sanger sequencing method at Genespec, Kakkanad.

A single sequence was generated and the trimmed sequences were edited with Bioedit v. 7.7.1(ref. 26) and subsequently aligned using ClustalW[27]. Sequence data were submitted to GenBank. There were a total of 674 positions in the final dataset. Evolutionary analyses were performed in MEGA11(ref. 28). For the maximum likelihood analysis, 1,000 bootstrap replicates were conducted using Kimura 2-parameter model with the Gamma distributed (G) distance and likelihood-ratio tests to choose the best-fit model[29]. Genetic distance was calculated using the Kimura 2-parameter (K2P) model[29].

Results

Taxonomic classification

Phylum: Chordata Haeckel, 1874
Class: Actinopterygii Klein, 1885
Order: Perciformes Bleeker, 1863
Family: Mullidae Rafinesque, 1815
Genus: *Mulloidichthys* Whitley, 1929
Mulloidichthys ayliffe Uiblein, 2011 (Fig. 2)

Material examined

Four specimens; SL 123 – 155 mm (Table 1); location: Agatti, Lakshadweep (10°48'40.9" N, 72°9'56.6" E); 5 – 10 m depth; collection method: shore seine; collection date: December 12, 2020. Vouchered specimen: GB.31.95.1.3, 143 mm SL (collection data same as above).

Diagnosis

D VIII+9; A I+6; V I+5; LI 37; total vertebrae 23 (Fig. 3).

Pectoral fin rays 16; gill rakers 7 – 8 + 19 – 20 (total 27 – 28): body slender and elongated with pointed snout, the depth at first dorsal-fin origin 24 – 26 % SL (standard length); body depth at anal fin origin 21 – 22 % SL; head length 28 – 30 % SL; maximum head depth 22 – 24 % SL; pelvic-fin length 20 – 22 % SL; pectoral-fin length 19 – 21 % SL; snout length 38.2 – 40.1 % HL (head length); barbel length 60.2 – 68.9 % HL; orbit length 29.6 – 32.7 % HL; postorbital length 33.0 – 37.2 % HL; body yellowish with four to five blue stripe alternating with yellow stripes; yellow stripes wider than the blue stripes; dorso-mid-lateral stripe is the most prominent.

Description

Morphometric measurements (as ratio of SL; range with mean in parenthesis): Body depth at first dorsal-

Fig. 2 — *Mulloidichthys ayliffe* Uiblein, 2011; SL: 143 mm (GB.31.95.1.3); Date of collection: 10/12/20

Table 1 — Morphometric and meristic characters and wet weight of four *Mulloidichthys ayliffe* specimens from off Lakshadweep, and comparison with earlier records

	Present Study				Uiblein, 2011		
	Specimen				Range (min-max)	Types and Non-types	Number of specimen studied
	1	2	3	4			
Standard length (mm)	123	143	153	155	123-155	152-245	22
In percentage of standard length							
Body depth at first dorsal-fin origin	26	24	25	26	24-26	26-29	21
Body depth at anal-fin origin	21	22	22	22	21-22	23-25	22
Half body depth	20	19	20	21	19-21	20-24	21
Half body depth at anal fin origin	15	15	15	16	15-16	16-18	22
Caudal-peduncle depth	8.9	9.3	9.2	9.4	8.9-9.4	10-11	22
Caudal-peduncle width at position of CPD measurement	4.4	3.9	4.0	4.2	3.9-4.4	4.1-5.3	22
Maximum head depth	24	22	23	24	22-24	22-25	22
Head depth across a vertical midline through eye	18	17	17	18	17-18	17-20	22
Suborbital depth	8	9	10	9	8.0-10	9.0-11	22
Interorbital length	7.6	7.8	7.3	8.2	7.3-8.2	8.6-11	22
Head length	29	30	29	28	28-30	28-31	22
Snout length	12	11	11	11	11-12	11-13	22
Postorbital length	10.9	9.8	10.4	10.0	9.8-10.9	9.5-11	22
Orbit length, horizontal fleshy orbit diameter	9.6	8.7	8.7	8.6	8.6-9.6	6.9-8.5	22
Orbit depth, vertical fleshy orbit diameter	8.4	7.5	7.9	7.5	7.5-8.4	6.4-7.5	22
Upper-jaw length	9.7	9.4	8.3	8.9	8.3-9.7	9.0-11	22
Lower-jaw length	9.3	8.8	8.4	8.5	8.4-9.3	8.6-11	22
Snout width	6.9	6.4	5.7	6.3	5.7-6.9	7.3-10	22
Barbel length	18	20	20	19	18-20	19-23	22
Maximum barbel width	0.9	0.9	0.9	0.9	0.9	0.6-1.0	22
First pre-dorsal length	39	38	37	37	37-39	37-41	22
Second pre-dorsal length	65	63	63	63	63-65	64-68	22
Interdorsal distance	11	12	12	12	11-12	12-16	22
Caudal-peduncle length	19	19	19	18	18-19	19-22	22
Pre-anal length	66	65	61	65	61-66	63-69	22
Pre-pelvic length	32	31	30	32	30-32	30-36	22
Pre-pectoral length	32	31	29	30	29-31	30-34	22
Second dorsal-fin depth	22	22	23	23	22-23	24-26	22
Pelvic-fin depth	25	24	25	26	24-26	26-29	22
Pectoral-fin depth	18	17	18	17	17-18	18-21	22
Length of first dorsal-fin base	18	15	18	15	15-18	16-18	21
Length of second dorsal-fin base	15	14	14	14	14-15	14-15	22
Caudal fin length	30	32		28	28-30	28-31	18
Length of anal-fin base	13	11	12	12	11-12	10-13	22
Anal fin height	15	16	15	15	15-16	14-17	20
Pelvic-fin length	21	21	19	20	19-22	19-22	22
Pectoral-fin length	21	20	19	20	19-21	19-22	22
Width of pectoral-fin base	4.7	4.3	4.8	4.9	4.3-4.9	4.2-5.2	22
First dorsal-fin height	21	22			21-22	21-24	21
Second dorsal-fin height	15	16	13	15	13-16	14-17	22
Position of crossing point of blue dorso-mid-lateral body stripe and lateral line	55	55			55	55-60	12
Meristics							
Pectoral-fin rays	16	16	16	16	16	16-17	22

(*Contd*.)

Table 1 — Morphometric and meristic characters and wet weight of four *Mulloidichthys ayliffe* specimens from off Lakshadweep, and comparison with earlier records

	Present Study				Uiblein, 2011		
	Specimen				Range (min-max)	Types and Non-types	Number of specimen studied
	1	2	3	4			
Rudimentary gill rakers on upper limb	2	2	2	1	1-2	0-2	22
Developed gill rakers on upper limb	6	6	5	6	5-6	5-8	22
Developed gill rakers on lower limb	16	14	14	15	14-16	14-19	22
Rudimentary gill rakers on lower limb	4	6	6	5	4-6	3-7	22
Total gill rakers on upper limb	8	8	7	7	7-8	7-8	22
Total gill rakers on lower limb	20	20	20	20	20	19-23	22
Total gill rakers	28	28	27	27	27-28	27-31	22
Lateral line scales	37	37	37	37	37	35-37	22
Wet weight (g)	42.6	61.8	75.5	84.1	42.6-84.1	n.a	-

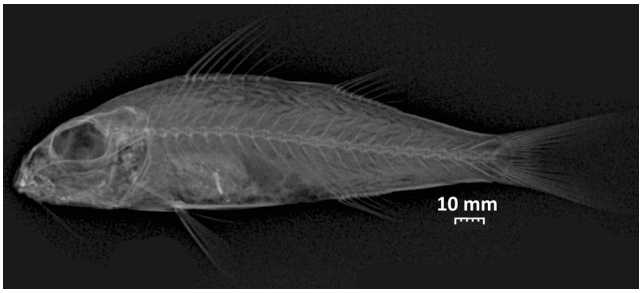

Fig. 3 — X-ray photography of *Mulloidichthys ayliffe*; SL: 143 mm (GB.31.95.1.3); Date of collection: 10/12/20

fin origin 3.8 – 4.2 (3.9), body depth at anal-fin origin 4.4 – 4.8 (4.6), maximum head depth 4.1 – 4.5 (4.3), head length 3.4 – 3.5 (3.4), snout length 8.5 – 9.3 (8.9), orbit length 10.4 – 11.7 (11.3), barbel length 4.9 – 5.7 (5.2), caudal peduncle length 5.1 – 5.4 (5.3), pelvic-fin length 4.6 – 5.2 (4.9), pectoral fin length 4.9 – 5.2 (5.0), anal fin height 6.4 – 6.9 (6.7), first dorsal-fin height 4.6 – 4.8 (4.7), second dorsal-fin height 6.2 – 7.4 (6.8). Morphometric and meristic data is provided in Table 1.

Head with small mouth; maxilla ends a little in front of orbit; upper jaw length ranges 8.3 – 9.7 times in standard length (SL); teeth small, conical in outer row and in an irregular pattern behind first row, teeth absent on vomerum and palate. Anterior nostril a small vertical opening, a little ahead of eye; posterior nostril is a narrow slit covered by a small membrane, placed near the edge of upper orbit; a single flat spine at the posterior edge of the operculum, at the mid-level of the eye; cycloid scales present on snout and chin regions; ctenoid scales present in other areas, fins naked except at the base of the caudal fin.

Colour in fresh fish

Body and head predominantly yellowish with four straight bluish lateral body stripes alternating with yellow stripes; yellow mid lateral stripes are wider than the bluish stripes; dorsolateral stripe not continuous, appearing as a series of small blue spots from behind the operculum to halfway along the body, passing just below the first dorsal fin base; dorso-midlateral stripe continuous, runs from behind the upper edge of the eye to below the rear end of the soft dorsal fin; ventro-mid lateral stripe runs in a straight line, origins from the snout tip, continuing below the eye as a curve line, and extending from behind the lower edge of the eye to behind the anal fin base. Ventro-lateral stripe placed below the ventro-mid lateral stripe, forming a straight line originating from the head, passing below the pectoral fin base to the tail; anterior and dorsal parts of body orange in freshly collected fish; head and body of preserved fish pale-brown. Ventral side of body whitish; caudal fins bright yellow, dorsal and anal fins pale yellow, pelvic fins yellowish posteriorly and whitish anteriorly; barbels white; outer jaw margins pale bluish white; the colour pattern showed no variation between samples. Colouration and patterning were congruent with the published description of *M. ayliffe*[4].

Molecular analysis

The sequence generated for *M. ayliffe* has been submitted to GenBank with accession number OQ921766. The *COI* gene sequence of *M. ayliffe* was compared with the closest sequences available in the NCBI database. The phylogenetic tree constructed using the Maximum Likelihood (ML) algorithm (Fig. 4) shows that the *COI* gene sequence of the present study closely related to sequences submitted for *M. ayliffe* from South Africa (Table 2). The ML consensus trees predicted the existence of two major clades, A and B. Clade A is constituted by *M. ayliffe* and a divergent clade, with *M. martinicus*,

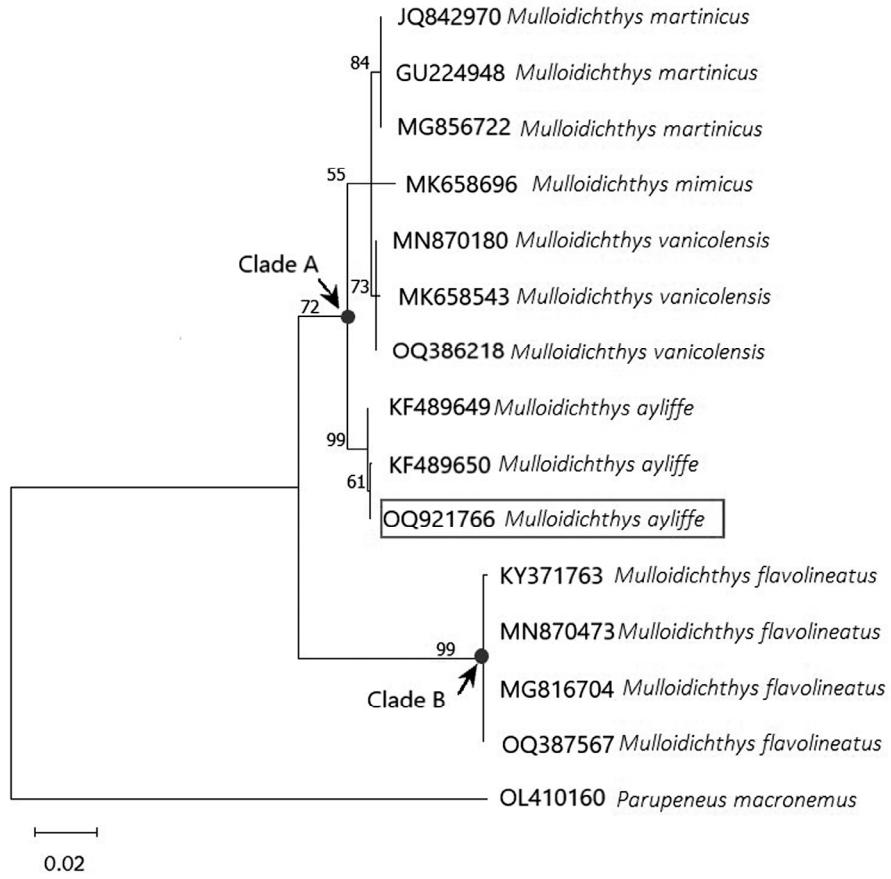

Fig. 4 — Maximum Likelihood (ML) tree based on the mtDNA *COI* gene sequences from various Mullidae species, including the newly generated sequence of *Mulloidichthys ayliffe*. Bootstrap values are shown above the branches, indicating the level of support for each node

Table 2 — Sequence used for phylogenetic tree analysis

Species	Geographical origin	Accession No	Sequence source
Parupeneus macronemus	Madagascar	OL410160	GenBank
Mulloidichthys flavolineatus	Philippines	OQ387567	GenBank
	Indonesia	MN87043	GenBank
	Hawaii	MG816704	GenBank
	China	KY371763	GenBank
Mulloidichthys vanicolensis	Philippines	OQ386218	GenBank
	Indonesia	MN870180	GenBank
	French Polynesia	MK658543	GenBank
Mulloidichthys ayliffe	Lakshadweep	OQ921766	Current study
	South Africa	KF489650	GenBank
	South Africa	KF489649	GenBank
Mulloidichthys martinicus	Yucatan Peninsula	GU224948	GenBank
	USA	MG856722	GenBank
	Caribbean	JQ842970	GenBank
Mulloidichthys mimicus	French Polynesia	MK658696	GenBank

M. mimicus and *M. vanicolensis* as its sister taxons. Clade B is constituted by *M. flavolineatus.* Genetic distances among *Mulloidichthys* species and the outgroup species, *P. macronemus* were calculated for *COI*. The phylogenetic tree for *Mulloidichthys ayliffe* was also constructed using the Neighbor-Joining (NJ) algorithm and is shown in Figure 5.

Value for interspecific genetic distances within the genus *Mulloidichthys* for *COI* ranged from 0.004 to 0.076, with an average of 0.035. The average K2P

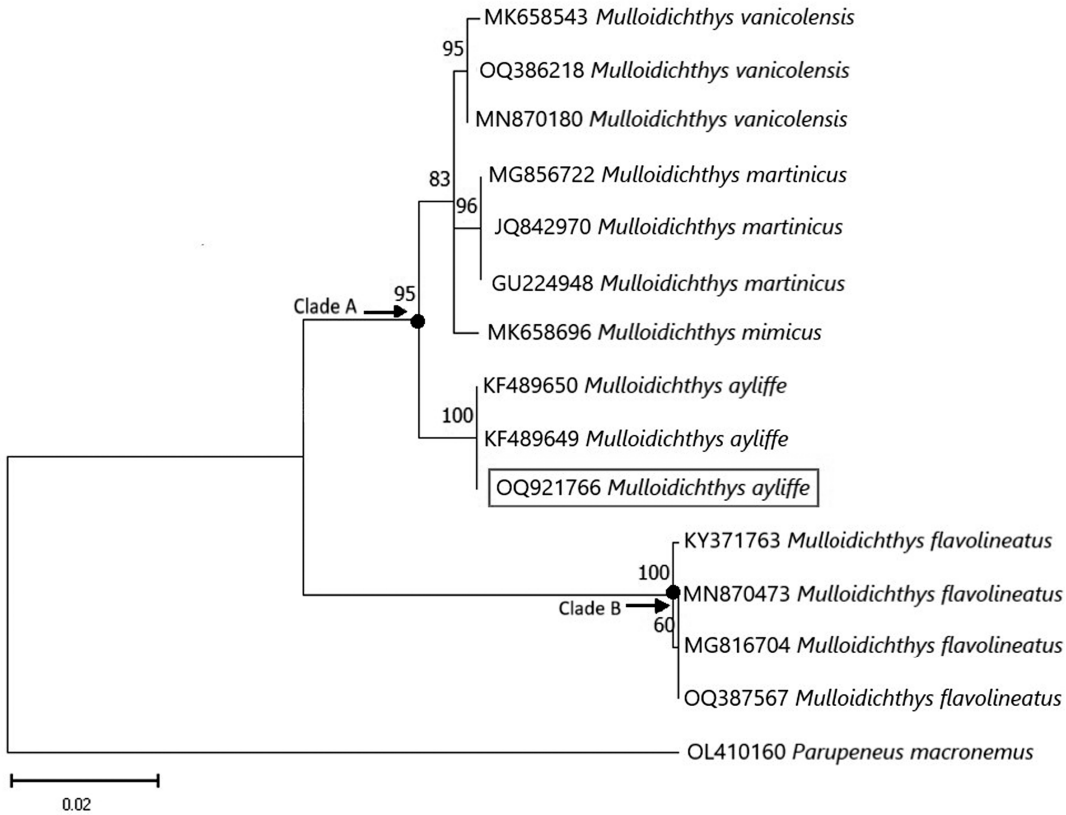

Fig. 5 — Neighbor-Joining tree (NJ) tree based on mtDNA *COI* gene of different Mullidae species along with the sequence generated of *Mulloidichthys ayliffe*

Table 3 — Interspecific Kimura 2-parameter (K2P) distance values for the six goatfish species for the *COI* gene

Species	***P. Macronemus***	***M. flavolineatus***	***M. vanicolensis***	***M. martinicus***	***M. mimicus***
P. marconemus	-				
M. flavolineatus	0.176	-			
M. vanicolensis	0.148	0.073	-		
M. martinicus	0.148	0.076	0.004	-	
M. mimicus	0.154	0.074	0.006	0.005	-
M. ayliffe	0.155	0.068	0.015	0.015	0.016

distance between *Mulloidichthys* species and the outgroup species ranged between 0.148 and 0.176. The average K2P distances within the *M. ayliffe* species ranged from 0.000 to 0.002. The maximum interspecific distance observed was between *M. martinicus* and *M. flavolineatus* (Table 3). Since no other sequence of *M. ayliffe* is available, and the observed genetic distance closest to *M. ayliffe* of South Africa confirms the identity of specimen as *M. ayliffe.* The average K2P genetic distance of interspecies and intraspecies for the *COI* gene is provided in Table 4.

Distribution: Indian Ocean: Natal, South Africa, Tanzania, Kenya, Oman, Seychelles, Sri Lanka, Andaman Islands[4] and Lakshadweep (present study).

Discussion

Species of the genus *Mulloidichthy*s can be distinguished based on their colour, meristic and morphometric characteristics. Body stripes are an important diagnostic characters[4]. Most of the *Mulloidichthys* species have dorso-midlateral body stripes. *Mulloidichthy*s *ayliffe* show close resemblance to *M. mimicus* in stripe pattern, with the colour of the stripes ranging from blue to pale blue. It differs, however, from *M. mimicus* in the pattern of the dorsal-most blue stripe crossing the lateral line beyond the first dorsal fin base and presence of 37 or less lateral line scales versus 38 to 39 in *M. mimicus.* The yellow background body colouration in *M. ayliffe* and *M. mimicus* affects the contrast of the wide

Table 4 — The average K2P genetic distance of interspecies and intraspecies (bold) for the *COI* gene

		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**
1	*M. ayliffe*	-													
2	*M. ayliffe*	**0.002**	-												
3	*M. ayliffe*	**0.000**	**0.000**	-											
4	*M. martinicus*	0.019	0.017	0.015	-										
5	*M. martinicus*	0.017	0.015	0.016	**0.000**	-									
6	*M. martinicus*	0.019	0.017	0.015	**0.000**	**0.000**	-								
7	*M. mimicus*	0.024	0.022	0.017	0.009	0.005	0.009	-							
8	*M. vanicolensis*	0.017	0.016	0.013	0.005	0.005	0.005	0.009	-						
9	*M. vanicolensis*	0.020	0.018	0.016	0.006	0.007	0.006	0.010	**0.002**	-					
10	*M. vanicolensis*	0.017	0.016	0.013	0.005	0.005	0.005	0.009	**0.000**	**0.002**	-				
11	*M. flavolineatus*	0.072	0.070	0.067	0.075	0.080	0.075	0.075	0.069	0.075	0.070	-			
12	*M. flavolineatus*	0.074	0.073	0.070	0.078	0.080	0.078	0.076	0.072	0.075	0.072	**0.000**	-		
13	*M. flavolineatus*	0.074	0.072	0.069	0.077	0.080	0.077	0.076	0.072	0.076	0.072	**0.002**	**0.002**	-	
14	*M. flavolineatus*	0.072	0.070	0.067	0.075	0.080	0.075	0.075	0.070	0.075	0.070	**0.000**	**0.000**	**0.002**	-
15	*P. macronemus*	0.158	0.158	0.156	0.149	0.151	0.149	0.153	0.150	0.156	0.151	0.177	0.178	0.179	0.178

yellow bands, making them less noticeable compared to other *Mulloidichthys* species. This also indicates that in these species, the perceived contrast of the stripes can be influenced by both the background and the overall body colour. The present specimen of *M. ayliffe* has four narrow pale blue continuous stripes with wider yellow band areas in between.

The comparison of morphometric data collected from *M. ayliffe* caught off Lakshadweep shows slight variation with the results by Uiblein[4], which were based on mostly much larger specimens (123 – 155 mm vs 152 – 245 mm SL) and hence may indicate allometric effects. Size-related variation in body shape is rather common in goatfishes and has been demonstrated by Uiblein[4] for *M. mimicus.*

Analysis of the meristic characters of the samples and comparison with other types and nontypes pointed to the confirmation of the identity of the species. The fin formula of the present specimen is in tandem with that of the holotype and paratypes (Table 1).

A single gene sequence (mitochondrial *COI*) of *M. ayliffe* was compared with two other sequences of *M. ayliffe* deposited at NCBI from South Africa, and no other sequence is available for comparison in NCBI. The blast alignment shows that the specimen was identical to the available sequences of *M. ayliffe*, confirming the occurrence of this species in Lakshadweep waters. Phylogenetic analysis of *M. ayliffe* revealed that *M. ayliffe* from South Africa belongs to the same clade that was recorded from Lakshadweep and forms a monophyletic clade with other sister species (Fig. 4). No information on *M. ayliffe* from Andaman is available. A maximum likelihood tree based on the mtDNA *COI* gene is given in Figure 4 with *Parupeneus macronemus* as outgroup. The present study, therefore, reports the extended geographical distribution of *M. ayliffe* from Sri Lanka to the eastern coast of the Arabian Sea and adds to the diversity count of goatfishes, a still poorly studied group from Indian waters. The present work thus confirms the presence of *M. ayliffe* in Laccadive waters and provides valuable morphological and genetic information for future work. It also fills a distributional gap in the Western Indian Ocean.

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Conflict of Interest

The authors have no competing interests.

Ethical Statement

This article does not contain any experimental studies with animals performed by any of the authors, and all fish specimens were legally collected from the sea during scientific surveys.

Author Contributions

KMV: Data curation, investigation, and draft preparation; RJN: Supervision, investigation, validation, writing, review and editing of original draft; and ATS: Data curation, investigation,

and formal analysis. All authors made substantial contributions to the conception or design of the work.

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